

## News &amp; Comments

## Relationship Between Phylogenetic Groups of *Escherichia Coli* and Pathogenicity

Zhiqin Zheng

Birds are more vulnerable to *E. coli* infections due to unfavourable environmental circumstances in housing facilities, such as high dust concentrations or low temperatures, the infectious bronchitis virus, and prior mycoplasma infections. Virulence-associated and antimicrobial resistance genes discovered in the isolates of extraintestinal pathogenic *E. coli* (ExPEC), including strains from urinary tract infections, new-born meningitis, and sepsis in humans, are shared by APEC and ExPEC.

Recent investigations have concentrated on avian colibacillosis strains that fall within phylogroups B2 and F according to the updated Clermont scheme because of their potential to spread to humans through zoonotic transmission and serve as an etiologic agent for extraintestinal illnesses. From hens with colibacillosis, healthy chicken faces, and environmental samples collected from various farms, strains were recovered. To clarify the relationship between colibacillosis isolates, all isolates were divided into phylogroups.

In comparison to isolates connected to healthy chicken, those related to colibacillosis had a much greater prevalence rate of phylogroup F. Furthermore, based on the presence of virulence-associated genes, 87 percent of the colibacillosis-related isolates within phylogroup F were classified as APEC. These findings suggest that colibacillosis may be mostly caused by isolates from phylogroup F, which are likely to be very virulent to hens. Furthermore, given that only 37 pulsotypes were identified in 104 *E. coli* isolates from chickens with colibacillosis, it is likely that isolates with a single pulsotype caused many infections. In contrast, PFGE analysis revealed that most of the isolates connected to healthy chicken were unique from one another, authors proclaimed.

Most healthy chicken-associated *E. coli* isolates with a low frequency of virulence-associated genes were categorized into phylogroups A and B1, while colibacillosis-related *E. coli* isolates tended to be predominately phylogroup F and virulence-associated genes. "Lethality of chicken embryos in the assay for chicken embryo lethality appeared to be correlated with the origin of the isolates; however, we cannot completely rule out the possibility that the small number of farms and the short time span used to collect the various samples in the current study had an impact on the distribution of phylogroups among *E. coli* isolates." Author Zhunge added. However, it is interesting that phylogroup F was predominate in colibacillosis-infected layer and broiler chickens. According to the author Wang, Phylogroup F detection may aid in the prediction of extremely virulent APEC.



**Journal Reference**

Murase T. and H. Ozaki, 2022. Relationship between phylogenetic groups of *Escherichia coli* and Pathogenicity among Isolates from chickens with Colibacillosis and healthy chickens. *Poult. Sci.*, 101: 102007. <https://doi.org/10.1016/j.psj.2022.102007>

**KEYWORDS**

Chicken, colibacillosis, *Escherichia coli*, phylogroup, virulence

